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13. Abstract *(Maximum 200 Words)* *(abstract should contain no proprietary or confidential information)*
This project is testing the hypothesis that breast cancer in elderly women represents a disease different than breast cancer in young women. The hypothesis is being tested using gene expression profiles as objective measures of breast cancer phenotypes. The study is being conducted using samples from Korean women because this likely represents a relatively homogeneous population from genetic and cultural perspectives. The proposed first phase of the project is to identify genes that are differentially expressed in a small set of breast cancers from young and elderly women. While we have been technically successful in conducting these studies as proposed, we have not found consistent differences in gene expression patterns between cancers from young and elderly patients. The second phase of this project is to construct a custom array that represents candidate genes for differentiating the cancers from young and elderly women. We will begin constructing this array soon, using genes that are differentially expressed among different breast cancers. Subsequent experiments will measure gene expression profiles in additional samples of breast cancers from Korean women and ultimately North American women.

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Introduction

Epidemiological studies that attempt to identify risk factors and causes of breast cancer commonly consider breast cancer to be a single disease and, thus, a single outcome. This approach probably prevents us from recognizing and accurately assessing important breast cancer risks and causes.

This project is testing the hypothesis that populations of women with significantly different demographic characteristics may not only have different incidences of breast cancers, but also different types of breast cancers. We are testing this hypothesis by examining breast cancers from two populations that differ apparently by only a single major variable: age. Specifically, we are using custom cDNA arrays to profile gene expression in breast cancers from young and elderly Korean women. Recently published studies using gene expression arrays to analyze breast cancers have shown that this approach has great potential for classifying breast cancer at the molecular level . We are using breast cancers from Korean women for the studies of our project because there is much less genetic and cultural diversity in the Korean population compared to the North American population.

Body

The work conducted in the first year of this project is following the timetable outlined in the Statement of Work. An initial series of breast cancers from Korean women (4 elderly and 4 young) have been analyzed using commercially prepared cDNA arrays from Incyte and Research Genetics. We have analyzed this data and we have identified a set of approximately 1800 genes with at least 2-fold variation in expression between at least two samples. We have not, in this small set of samples, recognized any consistent pattern that differentiates the breast cancers from young and elderly women.

Subsequent to these preliminary experiments to identify candidate genes, we have amplified cDNA clones for constructing custom arrays. Approximately 150 of these clones have not been successfully amplified, which is consistent with our previous experience with cDNA clone sets. Custom arrays have been printed that represent 1960 genes, including our candidate genes from the experiments of this project (~ 1650 genes) and other genes known to be involved in cancer-related processes (~ 250 genes).

During the first year of the project, we have also microdissected 18 cases of breast cancer (task 2 of SOW). These samples will be analyzed for gene expression using the custom arrays in the coming year.

Key Research Accomplishments

The construction of custom cDNA arrays is progressing as projected in the original application.

Reportable Outcomes

There are no reportable outcomes to date.

Conclusions

The project is progression as projected in the Statement of Work of the original application.

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Appendices

None